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SEQUENCE LISTING

Re/12
RE/12

<110> SUNTORY LIMITED

<120> Gene encoding a protein having aurone synthesis activity

<130> G837

<150> JP 10-107296

<151> 1998-04-17

<160> 15

<210> 1

<211> 1951

<212> DNA

<213> Antirrhinum majus

<220>

<221> CDS

<222> (96)...(1781)

<223> Nucleotide sequence encoding a protein having aurone synthesis activity

<400> 1

aaattacatt gtttccttgc tccccacccat caccaccaat atataacaact tcctcagcta 60

gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat 113

Met Phe Lys Asn Pro Asn

1

5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161

Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu

10

15

20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209

Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe

25

30

35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc	257		
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg			
40	45	50	
ttt gcc tcg acc tca acc ggc cct atc gcc gcc oct gat gtc acc aaa	305		
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys			
55	60	65	70
tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt	353		
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys			
75	80	85	
ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc	401		
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser			
90	95	100	
act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac	449		
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr			
105	110	115	
att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag	497		
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu			
120	125	130	
gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac	545		
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr			
135	140	145	150
tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa	593		
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln			
155	160	165	
atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac	641		
Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr			
170	175	180	
ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct	689		
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala			
185	190	195	
ctc cca ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca	737		
Leu Pro Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser			
200	205	210	
atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt	785		
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser			
215	220	225	230
aat cat cag cca cca acc atc gta gac ttg aac tac gac ttt tct gat	833		
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp			
235	240	245	

tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa			881
Ser Asp Asn Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys			
250	255	260	
att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc			929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe			
265	270	275	
ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg			977
Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly			
280	285	290	
tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct			1025
Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser			
295	300	305	310
gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct			1073
Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala			
315	320	325	
aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg			1121
Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp			
330	335	340	
tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat			1169
Ser Ile Trp Lys Thr Leu Gly Pro Arg Arg Thr Asp Leu Thr Asp			
345	350	355	
cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag			1217
Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu			
360	365	370	
atg gtt ccg gtc aag gtt ccg gat tgc tta gat gaa aag aaa cta ggg			1265
Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly			
375	380	385	390
tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca			1313
Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr			
395	400	405	
cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act			1361
Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr			
410	415	420	
gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa			1409
Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys			
425	430	435	
gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac			1457
Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp			
440	445	450	

gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac			1505
Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp			
455	460	465	470
cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac			1553
His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp			
475	480	485	
ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg			1601
Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val			
490	495	500	
agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta			1649
Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu			
505	510	515	
tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa			1697
Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu			
520	525	530	
gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg			1745
Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala			
535	540	545	550
atc aag att cat aat gtc aag att gag ctt gat ggc taataaaattc			1791
Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly			
555	560	562	
tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaaagta			1851
tctcatgtac caatatcgat cgtattaatc gtaataacttt cagattttta tttatcaa			1911
agcagttgta taaatggta aataaggatt actttttgag			1951

<210> 2

<211> 562

<212> PRT

<213> *Antirrhinum majus*

<220>

<223> Amino acid sequence of a protein having aurone synthesis activity

<400> 2

Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser

1

5

10

15

Asn	Asp	Asn	Asp	Gln	Glu	Ser	Ser	His	Arg	Cys	Lys	His	Ile	Ile	Leu	Leu
						20				25					30	
Phe	Ile	Ile	Thr	Leu	Phe	Leu	Leu	Ile	Val	Gly	Leu	Tyr	Ile	Ala	Asn	
						35			40			45				
Ser	Leu	Ala	Tyr	Ala	Arg	Phe	Ala	Ser	Thr	Ser	Thr	Gly	Pro	Ile	Ala	
						50		55			60					
Ala	Pro	Asp	Val	Thr	Lys	Cys	Gly	Gln	Pro	Asp	Leu	Pro	Pro	Gly	Thr	
						65		70		75			80			
Ala	Pro	Ile	Asn	Cys	Cys	Pro	Pro	Ile	Pro	Ala	Lys	Ile	Ile	Asp	Phe	
						85			90			95				
Glu	Leu	Pro	Pro	Pro	Ser	Thr	Thr	Met	Arg	Val	Arg	Arg	Ala	Ala	His	
						100			105			110				
Leu	Val	Asp	Asp	Ala	Tyr	Ile	Ala	Lys	Phe	Lys	Lys	Ala	Val	Glu	Leu	
						115		120			125					
Met	Arg	Ala	Leu	Pro	Glu	Asp	Asp	Pro	Arg	Ser	Phe	Lys	Gln	Gln	Ala	
						130		135			140					
Asn	Val	His	Cys	Ala	Tyr	Cys	Ala	Gly	Ala	Tyr	Asn	Gln	Ala	Gly	Phe	
						145		150		155			160			
Thr	Asn	Leu	Lys	Leu	Gln	Ile	His	Arg	Ser	Trp	Leu	Phe	Phe	Pro	Phe	
						165			170			175				
His	Arg	Tyr	Tyr	Ile	Tyr	Phe	Phe	Glu	Arg	Ile	Leu	Gly	Lys	Leu	Ile	
						180			185			190				
Asn	Asp	Thr	Thr	Phe	Ala	Leu	Pro	Phe	Trp	Asn	Tyr	Asp	Ser	Pro	Gly	
						195		200			205					
Gly	Met	Thr	Ile	Pro	Ser	Met	Phe	Ile	Asp	Thr	Asn	Ser	Ser	Leu	Tyr	
						210		215			220					
Asp	Ser	Leu	Arg	Asp	Ser	Asn	His	Gln	Pro	Pro	Thr	Ile	Val	Asp	Leu	
						225		230		235			240			
Asn	Tyr	Ala	Phe	Ser	Asp	Ser	Asp	Asn	Thr	Thr	Thr	Pro	Glu	Gln		
						245			250			255				
Met	Ile	Ile	Asn	Leu	Lys	Ile	Val	Tyr	Arg	Gln	Met	Val	Ser	Ser	Ala	
						260			265			270				
Lys	Thr	Pro	Gln	Leu	Phe	Phe	Gly	Arg	Pro	Tyr	Arg	Arg	Gly	Asp	Gln	
						275		280			285					
Glu	Phe	Pro	Gly	Val	Gly	Ser	Ile	Glu	Leu	Val	Pro	His	Gly	Met	Ile	
						290		295			300					
His	Leu	Trp	Thr	Gly	Ser	Glu	Asn	Thr	Pro	Tyr	Gly	Glu	Asn	Met	Gly	
						305		310		315			320			

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
325 330 335
Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
340 345 350
Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
355 360 365
Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
370 375 380
Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
385 390 395 400
Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
405 410 415
Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
420 425 430
Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
435 440 445
Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
450 455 460
Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
465 470 475 480
Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
485 490 495
Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
500 505 510
Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
515 520 525
Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
530 535 540
Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
545 550 555 560
Asp Gly
562

<210> 3
<211> 13
<212> PRT
<213> Antirrhinum majus

<220>

<223> Partial amino acid sequence of a protein having aurone synthesis activity

<400> 3

Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
5 10

<210> 4

<211> 12

<212> PRT

<213> Antirrhinum majus

<220>

<223> Partial amino acid sequence of a protein having aurone synthesis activity

<400> 4

Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
5 10

<210> 5

<211> 18

<212> PRT

<213> Antirrhinum majus

<220>

<223> Partial amino acid sequence of a protein having aurone synthesis activity

<400> 5

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
5 10 15
Glu Phe

<210> 6

<211> 30

<212> PRT

<213> *Antirrhinum majus*

<220>

<221> UNSURE

<222> (9)

<220>

<221> UNSURE

<222> (29)

<223> Partial amino acid sequence of a protein having aurone synthesis activity

<400> 6

<210> 7

<211> 125

<212> PRT

<213> *Antirrhinum majus*

<220>

<223> Partial amino acid sequence of a protein having aurone synthesis activity

<400> 7

Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe Phe Gly Arg
5 10 15

Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly Ser Ile Glu
30 35 30

Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr
35 40 45

Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro
50 55 60

Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp
67 70 75 80

Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe
85 90 95

Leu Asp Ala Ser Phe Val Phe Cys Asp Glu Asn Ala Glu Met Val Arg
100 105 110

Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly
115 120 125

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221>

<222> (2)

<223> Xaa is Val or Ile

<400> 8

Phe Xaa Lys Phe Thr Ala Ile

5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221>

<222> (6)

<223> Xaa is Thr or Pro

<400> 9

Lys Trp Lys Gly Lys Xaa

5

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221>

<222>

<223>

<400> 10

His Ala Val Cys Asn Glu

5

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223> Primer

<400> 11

ttyrtnaart tyacngcnat

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<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223> Primer

<400> 12

aartggaaarg gnaarmc

17

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<223> Primer

<400> 13
rtgngcnacr carttytc

18

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<223> Primer

<400> 14
aaggatccgg ccctatcgcc

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<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> Primer

<400> 15

gggttcgaag aattcatctc tg

22